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Long noncoding RNAs in hepatitis B virus replication and oncogenesis

Hui-Chun Li, Chee-Hing Yang, Shih-Yen Lo

Abstract

Several diverse long noncoding RNAs (lncRNAs) have been identified to be involved in hepatitis B virus (HBV) replication and oncogenesis, especially those dysregulated in HBV-related hepatocellular carcinoma (HCC). Most of these dysregulated lncRNAs are modulated by the HBV X protein. The regulatory mechanisms of some lncRNAs in HBV replication and oncogenesis have been characterized. Genetic polymorphisms of several lncRNAs affecting HBV replication or oncogenesis have also been studied. The prognosis of HCC remains poor. It is important to identify novel tumor markers for early diagnosis and find more therapeutic targets for effective treatments of HCC. Some dysregulated lncRNAs in HBV-related HCC may become biomarkers for early diagnosis and/or the therapeutic targets of HCC. This mini-review summarizes these findings briefly, focusing on recent developments.

Key Words: Hepatitis B virus; Hepatocellular carcinoma; Long noncoding RNAs; Hepatitis B virus X protein; Biomarker
Core Tip: The prognosis of hepatocellular carcinoma (HCC) remains poor. It is important to identify novel tumor markers for early diagnosis and find more therapeutic targets for effective treatments of HCC. Several diverse long noncoding RNAs (lncRNAs) have been identified to be involved in hepatitis B virus (HBV)-related HCC. A better understanding of the molecular mechanisms underlying lncRNA-mediated hepatocarcinogenesis may help for their use in early diagnosis and to identify appropriate targets for the prevention and treatment of HBV-related HCC.

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INTRODUCTION

Majority of the human genome (70%–90%) is actively transcribed. Only approximately 2% of these transcribed RNAs translate into proteins, while more than 90% of them are noncoding RNAs (ncRNAs). Based on size, ncRNAs are classified into small ncRNAs [less than 200 nucleotides (nt)] and long noncoding RNAs (lncRNAs, more than 200 nt). Several kinds of small ncRNAs have been characterized, including transfer-, ribo-, small nucleolar-, piwi -and miRNAs. It is well known that miRNAs (generally 22–25 nt) can regulate gene expression by suppressing protein translation or by mRNA degradation through interacting with their target mRNA sequences, usually at the 3’-untranslated regions (3’UTR). Various miRNAs have been found to be dysregulated and play important roles in hepatitis B virus (HBV) infection and hepatocellular carcinoma (HCC) progression[1].

LncRNAs are mostly transcribed by RNA polymerase II, sometimes polyadenylated and located in nuclear and/or cytosolic fractions. LncRNAs are divided into intergenic, intronic, bidirectional, sense, and antisense lncRNAs based on their genomic location and strand orientation. These lncRNAs may function as signals, decoys, guides, or scaffolds to regulate the expression of their target genes through interacting with their partner molecules[2]. In this way, lncRNAs can modulate gene expression at different levels, including epigenetic silencing, transcriptional control, post-transcriptional regulation, and protein stability modulation[2]. Thus, they are involved in many biological processes such as cell proliferation, invasion and metastasis, autophagy, and apoptosis. Indeed, dysregulation of lncRNAs has now been implicated in numerous human diseases, especially cancers, e.g., HCC[2].

Liver cancer was the sixth most common cancer and the third leading cause of cancer death in the world in 2020 (https://gco.iarc.fr/today/home). HCC represents approximately 90% of all cases of primary liver cancer. The leading cause of HCC is persistent HBV infection, which occurs in more than half of the HCC cases[3]. The management of HBV-related HCC has improved in the past decade. However, the outcome of HCC is still poor. Understanding more regarding the underlying mechanism of HBV-related HCC is required for improving the prevention, diagnosis, and treatment of HCC. The roles of lncRNAs in HBV-related HCC have received much more attention lately.

In this mini-review, we briefly outline the involvement of lncRNAs in HBV replication. We summarize the findings of dysregulated lncRNAs in HBV-related diseases, especially HCC, and discuss their roles and the potential clinical applications as diagnostic or therapeutic targets for HCC.

LNCRNAS IN HBV REPLICATION

HBV, belonging to the Hepadnaviridae family, is a small enveloped DNA virus. Ten HBV genotypes (A–J), which are based on eight percent or more sequence divergence across the viral genome, have been identified[4]. Even with the genotype differences, HBVs share the same pattern of replication cycle in the cells[5]. HBV infection begins with the attachment of virions to the surface proteoglycans on hepatocytes, followed by high affinity binding with more specific receptors (e.g., sodium taurocholate cotransporting polypeptide; NTCP)[6]. After entry into the cell, the viral compact, partially double-stranded genome (i.e., relaxed circular DNA) will form the stable covalently closed circular DNA (cccDNA) by viral and host factors[7]. Then, the viral RNAs [including sub-genomic mRNAs and pre-genomic RNA (pgRNA)] are transcribed from cccDNA using the cellular transcriptional machinery. The pgRNAs and the viral polymerase proteins (HBpAg) will be encapsidated by HBV core antigen (HBcAg) proteins. The newly formed nucleocapsids containing partially double-stranded HBV DNA made from pgRNA by HBpAg then either re-enter the nucleus to produce more cccDNA or release as mature virions following the assembly with HBV surface proteins (HBsAg)[5].
The 3.2 kilobases (kb) HBV genome contains four open reading frames (ORFs): Surface (S), precore (pre-C)/core (C), polymerase (P), and X. The S ORF encodes three viral envelope proteins initiated from different start codons: Large, middle, and small surface antigens (HBsAg). HBV ε antigen and core antigen (HBcAg) are encoded in the pre-C/C ORF[5]. The P ORF encodes viral polymerase (HBpAg) possessing reverse transcriptase, RNase H, and DNA polymerase activities. HBV X protein (HBxAg, HBx) derived from X ORF can transactivate the expression of both cellular and viral genes required for viral replication[5].

Nearly 257 million people worldwide have been infected with HBV, resulting in 887000 people dying of liver cirrhosis or HCC annually. Therefore, identification of new therapeutic targets against HBV is urgently needed. LncRNAs could be potential targets as a growing number of them have been found to play a role in HBV replication[8] (Figure 1).

LncRNAs facilitating HBV replication
LncRNA deleted in lymphocytic leukemia 2 (DLEU2): HBx was found to bind the DLEU2 promoter to enhance its transcription. Nuclear DLEU2 could directly bind to HBx or the histone methyltransferase enhancer of zeste homolog 2 (EZH2). The interaction of HBx and DLEU2 on the viral cccDNA displaces EZH2 from the viral chromatin to boost viral transcription and replication[9].

HOX transcript antisense RNA (HOTAIR): HOTAIR was significantly upregulated in HBV-infected cells. HOTAIR promoted HBV transcription and replication by elevating the activities of HBV promoters via modulation of the levels of cccDNA-bound SPI[10].

LncRNA proliferating cell nuclear antigen (PCNA) pseudogene 1 (PCNAPI): The expression levels of PCNAPI and PCNA were significantly elevated in the livers of HBV cccDNA-positive HCC patients. PCNA could interact with HBV cccDNA in a HBc-dependent manner. PCNAPI enhanced PCNA through sponging miR-154, which targets the 3’UTR of PCNA mRNA. Moreover, PCNAPI or PCNA enhanced HBV replication significantly both in vitro and in vivo. Thus, IncRNA PCNAPI enhances HBV replication through the miR-154/PCNA/HBV cccDNA axis[11].

LncRNA highly upregulated in liver cancer (HULC): The HULC gene is located on chromosome 6p24.3 and contains two exons and one intron. HULC is an IncRNA of around 500 nt mainly localized in the cytoplasm. HULC was found to elevate HBx, which coactivated STAT3 to stimulate the miR-539 promoter. Elevated miR-539, which targets the 3’UTR of APOBEC3B mRNA, downregulated APOBEC3B and promoted HBV replication. Thus, HULC activates HBV through the HBx/STAT3/miR-539/APOBEC3B axis[12]. Another study demonstrated that IncRNA HULC enhanced HBV replication through the HAT1/HULC/HBc complex responsible for the accumulation on cccDNA minichromosome[13]. Moreover, the HULC genetic variant rs7763881 is associated with HBV infection[14].

LncRNA zinc ribbon domain containing 1-antisense RNA 1 (ZNRD1-AS1): A ZNRD1, cloned from the human leukocyte antigen region, should play an important role in immune response against HBV infection. ZNRD1-AS1 is a strong regulator of ZNRD1. The variant allele of ZNRD1-AS1 (rs7757328) was reported to be associated with HBV clearance[15].

LncRNA HBx-long interspersed nuclear element 1 (HBx-LINE1): HBx-LINE1 suppresses miR-122 [16], a miRNA that has been demonstrated to inhibit HBV replication by directly targeting the HBV pgRNA sequence[17]. Thus, by depleting miR-122, HBx-LINE1 enhances HBV replication.

LncRNA AP000253: AP000253 was found to promote HBV transcription and replication in hepatoma cells[18]. However, the AP000253 expression in liver tissues and the molecular mechanism of its involvement in HBV infection are not clear yet.

LncRNAs suppressing HBV replication
LncRNA HOXA transcript at the distal tip (HOTTIP): HOTTIP is a 3764 nt transcript mapped to the HOXA locus. HOTTIP was found to be induced by HBV in vitro. Further studies demonstrated that HBpAg could bind to and stabilize cAMP-responsive element-binding protein 1 (CREB1) mRNA to facilitate its translation. Then, the CREB1 protein would bind to the regulatory element of HOTTIP to promote its expression. HOTTIP significantly suppresses HBV replication through its downstream factor HOXA13, which was found to bind to HBV Enh I/Xp to reduce the production of pgRNA as well as HBV replication. Thus, HBpAg attenuates HBV replication via activation of the CREB1/HOTTIP/HOXA13 axis. In this way, IncRNA HOTTIP could restrain HBV replication and contribute to viral persistent infection[19].

Other IncRNAs involved in HBV replication
H11, a novel inhibitor of La protein, suppressed HBV replication by blocking the interaction between La protein and HBV RNA. Further studies have shown that 61 IncRNAs were upregulated and 74 IncRNAs were downregulated in an H11 treatment group when compared with the control group[20]. These IncRNAs should affect HBV replication though further verification is required.

The importance of IncRNAs in HBV replication has started to emerge. However, many unidentified IncRNAs critical for HBV replication should exist, such as those regulated by HBx (mentioned in the following sections). HBx is required for transcription from the viral cccDNA minichromosome. Thus, HBx modulates HBV replication. The IncRNAs affected by HBx may modulate HBV replication. The
Li HC et al. LncRNAs in HBV replication and oncogenesis

Roles of these lncRNAs in HBV replication require further investigation.

LncRNAs in HBV-Related Immune Responses

The roles of lncRNAs in the host immune system during HBV infection have just started to emerge. LncRNA ENST00000519726 (lncRNA-HEIM) was highly expressed in monocytes and was further upregulated upon HBV infection. Elevated lncRNA-HEIM expression was remarkably correlated with the TGF-β signaling pathway. Furthermore, altering the endogenous lncRNA-HEIM amount in monocytes significantly affected TGF-β production. LncRNA FTX downregulates the expression of tumor necrosis factor-α (TNF-α), interleukin (IL)-6, IL-1β, and nuclear factor kB (NF-kB) but upregulates the expression of Tim-3. This result demonstrated the effect of FTX on the expression of inflammatory cytokines through FTX-miR-545-TIM3 axis.

High lncRNA-CD160 expression level can inhibit interferon (IFN)-γ and TNF-α secretion in CD8+ T cells and decrease the immune response of CD8+ T cells. LncRNA-CD160 can interact with histone-modification enzyme gene histone deacetylase 11 (HDAC-11) to form a complex on the promoters of IFN-γ and TNF-α to inhibit their expression. Thus, lncRNA-CD160 acts as an immune suppressor. Indeed, knockdown of lncRNA-CD160 can block HBV infection.

Lnc-DC is a specific group of lncRNAs in dendritic cells. Lnc-DC could be activated by HBV infection. In addition, Lnc-DC is important in regulating the growth, apoptosis, and immune response of dendritic cells mediated by TLR9/STAT3 signaling. Moreover, the regulation of Lnc-DC controlled the immune response by reduction in secreted TNF-α, IL-6, IL-12, and IFN-γ, while increasing the IL-1β concentration in dendritic cells.

LncRNA#32 could positively regulate IFN-stimulated gene expression by interacting with activating transcription factor 2. Indeed, depletion of LncRNA#32 resulted in a significant increase in the replication of several viruses, including HBV. Thus, LncRNA#32 plays a role in host antiviral responses.
The role of lncRNAs in the HBV-related immune responses remains unclear. There should be many unidentified lncRNAs important for HBV-related immune responses, such as those involved in HBV-related HCC.

LncRNAs in HBV-related Chronic Diseases

Progression of liver disease from chronic HBV infection to HCC may include several stages[26], such as fibrosis and cirrhosis (Figure 2). The roles of lncRNAs in these HBV-related chronic diseases are largely unknown.

Transforming growth factor-β (TGF-β) plays an important role in various pathogenic processes, from inflammation, fibrosis, and cirrhosis to cancer. LncRNA-ATB, which is activated by TGF-β, is a key regulator of the TGF-β signaling pathway. The plasma levels of lncRNA-ATB in HBV-related cirrhosis patients were significantly higher than those in healthy controls[27].

Serum lincRNA-p21 levels in CHB patients, those with hepatitis B cirrhosis, and HBV-related HCC, were higher than those in the control subjects. LncRNA-p21 level was negatively correlated with levels of HBV DNA, alanine aminotransferase, and aspartate aminotransferase in patients with liver diseases. Thus, serum lincRNA-p21 may serve as a potential biomarker for liver cell damage in patients with hepatitis virus infection, hepatitis B cirrhosis, and HBV-related HCC[28].

Compared with that in healthy controls, HBV carriers, and CHB patients, the expression of lnc-TCL6 was obviously upregulated in Child–Pugh A patients with liver cirrhosis. Thus, lnc-TCL6 was identified as a sensitive biomarker for early diagnosis of liver cirrhosis (Child–Pugh A)[29].

LncRNA metastasis associated in lung adenocarcinoma transcript 1 (MALAT1) expression in CHB group was significantly upregulated compared to the control group. Moreover, the thioredoxin interacting protein (TXNIP) was also significantly upregulated in the CHB group. Further studies indicate that the MALAT1/hsa-miR-20b-5p/TXNIP axis may mediate CHB-induced inflammatory damage in chronic HBV infection complicated with non-alcoholic fatty liver disease[30].

LncRNA-maternally expressed gene-3 (MEG3) was reported to be significantly downregulated in human HCC cell lines possibly due to the MEG3 promoter being hyper-methylated. Further studies indicated that the serum level of lncRNA-MEG3 was lower in CHB patients, which is negatively correlated to the liver fibrotic degree. In vitro experiments verified those results. Thus, lncRNA-MEG3 may serve as a diagnostic biomarker for CHB[31].

LncRNA growth arrest specific transcript 5 (GAS5) is significantly downregulated in CHB patients due to its promoter methylation. Compared with the sera of healthy controls, lower GAS5 levels were detected in the sera of CHB patients. Thus, lncRNA GAS5 is also reported as a biomarker for liver fibrosis in CHB patients[32].

CHB patients might progress to acute-on-chronic liver failure (ACLF) with a high fatality rate. Four lncRNAs (RP11-25K21.6, THR2, RAB27A, and GNPTAB) were found to be differentially expressed between the ACLF and the control groups. Aberrant lncRNAs might be used to develop novel diagnostic biomarkers and/or therapeutic targets for ACLF[33].

The role of lncRNAs in the HBV-related chronic diseases is not clear yet. Those lncRNAs involved in HBV-related HCC (mentioned in the following section) may also play roles in HBV-related chronic diseases. This requires further investigation.

LncRNAs Dysregulated in HBV-related HCC

HCC was the sixth most common cancer in world in 2020. Risk factors of HCC include external stimuli such as HBV or hepatitis C virus infection, intake of aflatoxin B1, alcohol consumption, smoking, and host factors such as age, gender, genetics, and comorbidities. Globally, approximately 2 billion people have been infected with HBV. Among them, more than 350 million people are chronic HBV carriers. Chronic HBV infection has been implicated in HCC development. In fact, persistent HBV infection occurs in more than half of HCC, particularly in developing countries. Comparing with other solid malignancies, HCC is characterized by its highly invasive and metastatic potential. Indeed, HCC is the third leading cause of cancer death in world. This is in part due to the fact that patients may not exhibit symptoms at early stages of HCC[34]. Therefore, comprehensive approaches are warranted to identify novel tumor markers and find more effective therapeutic targets to improve the diagnosis and treatment of HCC[8]. In recent years the idea has emerged that regulatory ncRNAs, such as miRNAs and lncRNAs, should play regulatory roles in cancers such as HCC[1]. Specifically, various lncRNAs were reported to regulate the expression of tumor suppressor genes or oncogenes involved in cancer development[2].

HCC caused by HBV infection is related to different HBV genotypes, the mutation status of viral genomes, integration of viral DNAs, and the dysregulation of signaling pathways affected by HBV. However, the detailed mechanisms of HBV-related HCC remain to be determined. The development of
Hepatitis B virus (HBV) replication and oncogenesis

**UPREGULATED lncRNAs in HBV-related HCC**

**HULC**

HULC was the first lncRNA reported to be specifically upregulated in HCC through microarray analysis and quantitative reverse transcriptase polymerase chain reaction (qRT-PCR). By interacting with CREB, HBx up-regulates the HULC expression in hepatoma cell lines and HBV-related HCC tissues. HULC downregulates the expression of p18, a tumor suppressor gene close to HULC, and thus promotes the proliferation of hepatoma cells[42]. Moreover, HULC can act as a molecular sponge for miR-107. By sponging miR-107, HULC upregulates E2F1 and then activates SPHK1 transcription in hepatoma cell lines and HBV-related HCC tissues. Thus, HULC promotes tumor angiogenesis through miR-107/E2F1/SPHK1 signaling[43]. Altogether, these studies indicate that HULC serves as an oncogene important for HBV-related HCC. HULC is also demonstrated to act as an endogenous ‘sponge’ for various other miRNAs (e.g., miR-372, miR-186, miR-488, miR-200a-5p, miR-6825-5p, miR-6845-5p, and miR-6886-3p) in hepatoma cell lines and HCC tissues[44]. Those findings provide new insights into the mechanism of HULC in the HCC development (Table 1).
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<td>HULC[43]</td>
<td>Sequesters microRNAs and decreases p18 expression</td>
<td>Promotes proliferation of hepatoma cells and tumor angiogenesis in vitro and in vivo</td>
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<td>HOTAIR[45,47]</td>
<td>Suppresses miRNA-218 expression and inactivation of P14 and P16 signaling</td>
<td>Promotes migration and invasion of HCC cells</td>
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<td>HEIH[48]</td>
<td>Binds to EZH2 and represses EZH2 targets</td>
<td>Promotes cell proliferation and tumor growth, modulates cell cycle</td>
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<td>HBx-LINE1[16,49]</td>
<td>Sequesters miR-122 and activates Wnt signaling pathway</td>
<td>Promotes cell motility through EMT</td>
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<td>UCA1[53,54]</td>
<td>Through the HBs/UCA1/EZH2/p27 axis in nucleus; sequesters miR-216b and miR-203 in cytoplasm</td>
<td>Promotes growth, metastasis, and EMT of HCC cell lines</td>
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<td>DBH-AS1[56]</td>
<td>Activates the ERK/p38/JNK MAPK signaling pathway</td>
<td>Inhibits serum starvation-induced apoptosis of HCC cells, promotes tumor growth, proliferation, and cell-cycle progression of HCC cells</td>
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<td>HOTTIP[57]</td>
<td>Upregulates the expression of HOXA genes (e.g., HOX A10, 11, and 13)</td>
<td>Inhibits proliferation and migration of HCC cells in vitro and reduces tumorigenesis and pulmonary metastasis in vivo</td>
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<td>ANRIL[59,60]</td>
<td>Represses the KLF2 transcription through binding to PRC2; serves as a molecular sponge for miR-122-5p</td>
<td>Inhibits proliferation of HCC cells in vitro and promotes proliferation, invasion, and migration of HCC cells in vitro</td>
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<td>LINC00152[61]</td>
<td>Inhibits the expression of E-cadherin; activates the mTOR pathway</td>
<td>Promotes the proliferation and EMT of HCC cell lines and tumorigenesis</td>
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<td>MALAT1[63,66]</td>
<td>Upregulates LTBP3 transcription</td>
<td>Promotes migration and invasion of HCC cells in vitro and tumor growth in vivo</td>
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<td>Production of miR-545/374a</td>
<td>Promotes tumor progression</td>
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<td>Activates angiogenesis through reducing the secretion of PGK1</td>
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<td>Unigene56159[69]</td>
<td>Sequesters miR-140-5p</td>
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<td>n335586[73]</td>
<td>n335586/miR-924/CKMT1A axis</td>
<td>Contributes to cell migration and invasion</td>
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<td>TRERNA1/miR-22-3p/NRAS axis</td>
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<td>IncRNA IHS[80]</td>
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<td>Promotes tumor proliferation and metastasis in HCC</td>
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<td>SNHG20[81]</td>
<td>Negatively regulated PTEN protein level</td>
<td>Facilitates the proliferation of HCC cells</td>
</tr>
<tr>
<td>AX800134[82]</td>
<td>Not known</td>
<td>Antiapoptosis</td>
</tr>
</tbody>
</table>

LncRNAs: Long noncoding RNAs; HCC: Hepatocellular carcinoma; EMT: Epithelial-to-mesenchymal transition; HULC: Highly upregulated in liver cancer; HBV: Hepatitis B virus; HBx: HBV X protein; LINE: Long interspersed nuclear elements; HOTTIP: HOXA transcript at the distal tip; HOTAIR: HOX transcript antisense RNA; GAS5: Growth arrest specific transcript 5; MEG3: Maternally expressed gene-3; MALAT1: Metastasis associated in lung adenocarcinoma transcript 1; PGK1: Phosphoglycerate kinase 1.

**HOTAIR**

The *HOTAIR* gene is on chromosome 12. LncRNA HOTAIR is a 2158 nt transcript derived from the *HOTAIR* gene. HOTAIR is involved in the occurrence of HBV-related HCC. HBV replication and, in particular, HBx production, stimulates expression of HOTAIR and Plk1. The combination of Plk1 and HOTAIR is involved in epigenetic reprogramming associated with oncogenic transformation[45]. In *vitro* studies have demonstrated that HOTAIR has sequence-specific effects and interacts with various chromatin modifying proteins, e.g., Polycomb repressive complex 2 (PRC2)[46]. Another study showed
that HOTAIR might mediate hepatocarcinogenesis by down-regulating miR-218 and in-activating P14 and P16 signaling[47]. These findings suggest that lncRNA HOTAIR should play an important role in hepatocarcinogenesis (Table 1).

High expression in HCC

The high expression in HCC (HEIH) gene is on chromosome 5. LncRNA HEIH is a polyadenylated, approximately 1600 nt in length, lncRNA, whose expression is strongly linked to HBV-associated HCC. It is located both in the nucleus and cytoplasm. HEIH could promote cell proliferation by upregulating PCNA and decreasing the expression of p16, p21, and p27 in cells. Moreover, HEIH could promote tumor growth in nude mice. Mechanistically, HEIH is physiologically associated with EZH2, the catalytic subunit of the PRC2. The association of HEIH with EZH2 is needed to repress the EZH2 target genes[48]. These studies demonstrate that HEIH contributes to HBV-related HCC through the participation of epigenetic silencing (Table 1).

HBx-LINE1

Almost all HBV-related HCC tumors (85%-90%) have at least one HBV insertion site in the host genome. Thus, integration of HBV DNA should be important for the HCC development. LINEs appear to be a favored site for HBV DNA integration. To investigate the effect of HBV integration on genome disruption, HBx-LINE1, a viral-human chimeric fusion transcript derived from viral sequences containing HBx and cellular LINEs, was found functioning as an lncRNA. HBx-LINE1 was detected in 23.3% of HBV-related HCC patients[49,50]. HBx-LINE1, on chromosome 8p11.21, was transcribed from the HBx promoter. HBx-LINE1 contains six miR-122-binding sites and serves as a molecular sponge to sequester cellular miR-122. By downregulating miR-122, HBx-LINE1 activates the β-catenin signaling pathway, and in turn enhances HCC cell proliferation, invasion, and migration[16]. However, these findings were not consistent with those from other studies[51]. More studies with a larger sample size should help further clarify the role of HBx-LINE1 in the HBV-related HCC (Table 1).

Urothelial carcinoma associated 1

The urothelial carcinoma associated 1 (UCA1) gene is approximately 7.3 kb in length on chromosome 19p13.12 and contains three exons. It has three transcriptional isoforms. UCA1, around 1400 nt in length, is the most abundant isoform of the UCA1 gene[52]. UCA1 was originally identified in the bladder cancer cell line and also played an important role in HBV-related HCC. HBx can upregulate UCA1 expression[37,53]. UCA1, an lncRNA detected in both the cytoplasm and nucleus[53], has diverse functions. In nucleus, UCA1 recruits EZH2 to the p27 promoter, reduces the p27 expression, and enhances CDK2. Thus, UCA1 could promote the growth of hepatic and hepatoma cells through the HBx/UCA1/EZH2/p27 axis[53]. In cytoplasm, UCA1 serves as a molecular sponge for miR-216b and miR-203. Through sequestering miR-216b, UCA1 could promote the growth and metastasis of HCC cell lines by up-regulating the expression of fibroblast growth factor receptor 1 and activating the extracellular signal-regulated kinase signaling pathway[54]. In addition, sequestering miR-203 facilitates epithelial-to-mesenchymal transition (EMT) in HCC cells through Snail2 upregulation[55]. Thus, UCA1 could promote cell cycle progression, enhance cell proliferation, and decrease cell apoptosis in HBx-related HCC[37] (Table 1).

DBH-AS1

DBH-AS1 is an lncRNA of approximate 2 kb located on chromosome 9q34. HBx can upregulate the expression of DBH-AS1, which promotes HCC cell proliferation[37]. DBH-AS1 activates the ERK/p38/JNK MAPK signaling pathway. Once activated, ERK/p38/JNK MAPK can upregulate cyclin-dependent kinase 6 (CDK6), CCND1, and CCNE1 (members of cyclins) and downregulate p16, p21, and p27 (inhibitors of CDK). Thus, DBH-AS1 could induce the G1/S and G2/M transitions and promote cell proliferation. DBH-AS1 was also shown to protect HCC cells from serum starvation-induced apoptosis. These results suggested that DBH-AS1 acts as an oncogene[56]. However, a recent study showed contradicting results regarding the expression pattern of DBH-AS1[57]. To elucidate the exact role of DBH-AS1 in HBV-related HCC, more research is required (Table 1).

HOTTIP

LncRNA HOTTIP, a 3764 nt transcript, is located on chromosome 7p15.2 and encodes from a genomic region in the 5’ tip of the HOXA locus. LncRNA-HOTTIP was significantly overexpressed in tumor tissues compared to adjacent non-tumor tissues of the HCC patients. Patients with high HOTTIP expression were associated with increased metastasis formation and decreased overall survival. HOTTIP has also been detected to be upregulated significantly in HBV-related HCC patients[57]. Elevated HOTTIP expression could enhance cell proliferation and migration and contribute to metastasis of HCC partly by upregulating its neighboring HOXA genes (e.g., HOXA 10, 11 and 13), which are associated with various cancer types. These findings suggest that HOTTIP acts as an oncogene in HBV-related HCC (Table 1).
Antisense ncRNA in the INK4 locus

Antisense ncRNA in the INK4 locus (ANRIL), a 3800 nt lncRNA, is in the INK4BARF-INK4A gene cluster[58]. ANRIL is upregulated in several cancers including HBV-related HCC[57]. The ANRIL expression was associated with tumor size, histological grade, and overall survival in HCC patients[59]. These findings indicate that ANRIL plays a role in the HCC development, particularly HBV-related HCC. Knockdown of ANRIL expression in HCC cells in vitro could induce apoptosis and reduce the proliferation, invasion, and migration of these HCC cells[60]. Furthermore, inhibition of ANRIL led to slower tumor growth in vivo[59,60]. ANRIL represses the KLF2 transcription through binding with PRC2[59]. ANRIL also serves as a molecular sponge for miR-122-5p, whose overexpression significantly repressed the proliferation, migration, and invasion of HCC cells[60]. These findings indicate that ANRIL is also an oncogene in HBV-related HCC (Table 1).

LINC00152

LINC00152, an lncRNA of 828 nt, is mapped to chromosome 2p11.2 and contains four exons. It is mainly localized in the nucleus of HCC cells. The LINC00152 expression is associated with tumor size, HBV infection, and HBx amount[61]. Elevated LINC00152 expression also results in decreased overall survival[61]. LINC00152 is up-regulated by HBx protein and enhances proliferation and EMT of HCC cell lines in vitro and tumorigenesis in vivo[61]. LINC00152 has been shown to activate the mTOR pathway, which is a classic dysregulated pathway involved in the pathogenesis of HCC. In addition, LINC00152 promotes EMT by reducing the binding of EZH2 to the E-cadherin promoter and suppressing E-cadherin expression in HCC cell lines[61]. Ablation of E-cadherin will lose cell–cell contacts, resulting in EMT. These studies suggest that LINC00152 contributes to HBV-related HCC (Table 1).

Metastasis-associated lung adenocarcinoma transcript 1

Metastasis-associated lung adenocarcinoma transcript 1 (MALAT1) (also known as nuclear-enriched abundant transcript 2), an lncRNA of approximate 8000 nt in length, is mainly localized in the nucleus [62]. MALAT1 expression is elevated by HBx in HCC tissues and cell lines[63]. Sp1 and Sp3, also found upregulated, would bind to the proximal promoter region and enhance the transcription of MALAT1 [64]. MALAT1 affects alternative splicing and gene expression[62,65]. MALAT1 could promote tumor growth and metastasis by upregulating latent-transforming growth factor beta-binding protein 3 (LTBP3) expression. These results suggest that MALAT1 mediates the oncogenic effect of HBx through enhancing the LTBP3 expression, which promotes early metastatic events[63]. Moreover, a higher MALAT1 expression correlates to HCC recurrence after liver transplantation[66]. Additionally, knockdown of MALAT1 has been shown to reduce cell viability, motility, and invasiveness and increase sensitivity to apoptosis in HepG2 cells[66]. Therefore, MALAT1 is also an oncogene contributing to the risk of HBV-related HCC (Table 1).

Ftx

LncRNA Ftx is transcribed within the X-inactivation center[67]. Ftx encodes four miRNA clusters in its introns, among them, miR-545/374a located in intron b of Ftx has been implicated in HBV-associated HCC[22]. Expression of miR-374a and miR-545 was significantly higher in tumor tissues of HBV-related HCC. Further investigations suggested that miR-545/374a may contribute to poor prognosis by enhancing tumor invasion. This was supported by the observation that the proliferation of malignant cells was significantly suppressed in the presence of miR-545/374a inhibitors. On the other hand, overexpression of the miRNAs resulted in increased proliferation. miR-545/374a also enhanced migration and invasion abilities of HCC cells. Moreover, clinical samples positive for HBV DNA showed an increase in miR-545/374a. The upregulation of miR545 was also found to be HBx-dependent. Three targets for miR-545/374a were identified: Estrogen-related receptor alpha, estrogen-related receptor gamma (ESRRG), and arginine and glutamate rich. Experimental evidence demonstrated that miR-545 could downregulate ESRRG expression. Additionally, miR-374a had been shown to activate Wnt signaling pathway. In conclusion, lncRNA Ftx involves HBV-related HCC by serving as miRNAs precursor (Table 1).

Microvascular invasion in HCC

Microvascular invasion in HCC (MVIH) is situated within the intron of the ribosomal protein S24 gene. The MVIH expression was significantly upregulated in HBV-related HCC. Highly expressed MVIH was associated with frequent microvascular invasion and decreased overall survival[68]. Further investigations found that MVIH could promote tumor growth and metastasis by enhancing angiogenesis through reducing the secretion of phosphoglycerate kinase 1 suppressing angiogenesis[68] (Table 1).

Unigene56159

Unigene56159, an lncRNA of 2653 nt, is in the second intron of ROBO1. Unigene56159 was elevated in HBV-related HCC and HBV-producing cell line. Further investigations have found that Unigene56159, induced by HBV, could promote the EMT, migration, and invasion of hepatoma cells through seques-
LncRNAs in HBV replication and oncogenesis

**GENETIC POLYMORPHISMS OF LNCRNAS IN HBV REPLICATION AND ONCOGENESIS**

A number of dysregulated lncRNAs have been identified in HBV replication and oncogenesis[2,37]. Genetic polymorphisms affecting the expression (changes in the enhancer/promoter region) or activity (differences in the coding region) of these lncRNAs may also affect HBV replication and oncogenesis. Association studies are used to identify genetic variations of lncRNAs involved in HBV replication and oncogenesis[2].

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**DOWNREGULATED LNCRNAS IN HBV RELATED HCC**

**Downregulated expression by HBx**

Downregulated expression by HBx (Dreh), an lncRNA of approximate 700 nt in length, is mapped to chromosome 5. The Dreh expression was downregulated by HBx in HCC cell lines. Dreh is also significantly downregulated in HBV-related HCC tissues. Suppression of DREH facilitates proliferation of hepatoma cells in vitro and also tumor growth in vivo[84]. Lower Dreh expression is associated with the recurrence-free survival and overall survival of HCC patients[84]. Playing as a tumor suppressor in the development of HBV-related HCC, Dreh suppressed cell proliferation and cell migration in vitro and in vivo. By binding to the intermediate filament protein vimentin, lncRNA Dreh inhibits its expression and alters its filament structure to repress tumor cell migration. Therefore, HBx inhibits Dreh expression and in turn facilitates HCC (Table 2).

**Low expression in tumor**

LncRNA-low expression in tumor (LET) is an lncRNA identified to be decreased in HBV-related HCC. LncRNA-LET and nuclear factor 90 (NF90) are associated with each other. LncRNA-LET could downregulate NF90. NF90 has been implicated in the stabilization of many factors (e.g., hypoxia induced factor 1α [HIF-1α]) related to tumor growth and metastasis[85,86]. The LET/NF90/HIF-1α axis may be critical for HCC invasion in hypoxic environments. Under hypoxia conditions, induced HDAC-3 suppressed LET expression, which increased the expression of NF90 and HIF-1α, and, hence, enhanced the invasiveness of HCC and contributed to HCC progression[85].

In addition to the abovementioned lncRNAs, the expression of uc.306[87], UPAT[88], SEMA6A-AS1[89], BANCR[90], and miR143HG[91] was found to be decreased in HBV-related HCC. Moreover, the expression of lncRNA-6195[92], LINC01352[93], and F11-AS1[94] was suppressed by HBx. These downregulated lncRNAs by HBV and/or HBx serve as tumor repressors and suppress HCC cell proliferation (Table 2).

**OTHER LNCRNAS IN HBV-RELATED HCC**

**H19**

The H19 gene is located adjacent to the insulin-like growth factor 2 gene on chromosome 11p15.5. This gene produces a 2.3 kb lncRNA, which is exclusively expressed from the maternal allele. Reports of H19 expression in HCC are controversial. Recently, lncRNA H19 was found to be upregulated in CHB patients[95]. On the other hand, lncRNA H19 could suppress the growth of hepatoblastoma cells by promoting their apoptosis[96].

Most of these dysregulated lncRNAs are modulated by HBx, it would help to know whether altered versions of the preS/S envelope proteins would modulate the expression of lncRNAs or not. The progress of research on the role of lncRNAs in HBV-related HCC is impressive. However, the functions of a large proportion of lncRNAs dysregulated in HBV-related HCC remain elusive. Future investigation on the function of lncRNAs in HBV-related HCC will shed the light on understanding the detailed mechanisms regarding the development of HBV-induced HCC. Understanding more regarding the molecular mechanisms underlying lncRNA-mediated oncogenesis should help for their use in diagnosis and to identify appropriate targets for prevention and treatment of HBV-related HCC.
Table 2 Long noncoding RNAs downregulated in hepatitis B virus-related hepatocellular carcinoma

<table>
<thead>
<tr>
<th>LncRNA name</th>
<th>Regulatory mechanism</th>
<th>Biological function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dreh[84]</td>
<td>Inhibits the vimentin expression and alters its structure</td>
<td>Inhibits proliferation of HCC cells in vitro and tumor growth in vivo</td>
</tr>
<tr>
<td>LET[85]</td>
<td>LET/NF90/HIF1-a axis</td>
<td>Inhibits HCC invasion</td>
</tr>
<tr>
<td>uc.306[87]</td>
<td>May participate in the Wnt pathway</td>
<td>Not known</td>
</tr>
<tr>
<td>UPAT[88]</td>
<td>Promotes ZEB1 degradation</td>
<td>Suppresses cellular migration, invasion, and EMT processes</td>
</tr>
<tr>
<td>SEMA6A-AS1[89]</td>
<td>Not known</td>
<td>Not known</td>
</tr>
<tr>
<td>BANCR[90]</td>
<td>Not known</td>
<td>Not known</td>
</tr>
<tr>
<td>miR143HG</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LncRNA-6195</td>
<td>Represses the enzymatic activity of ENO1</td>
<td>Represses the growth of HCC</td>
</tr>
<tr>
<td>LINC01352</td>
<td>LINC01352/miR-135b/APC axis</td>
<td>Facilitates HCC progression</td>
</tr>
<tr>
<td>F11-AS1[94]</td>
<td>lncRNA F11-AS1/miR-211-5p/NR1I3 axis</td>
<td>Inhibits HCC growth and metastasis</td>
</tr>
</tbody>
</table>

LncRNAs: Long noncoding RNAs; HCC: Hepatocellular carcinoma; EMT: Epithelial-to-mesenchymal transition; HIF-1α: Hypoxia induced factor 1-α.

**GENETIC POLYMORPHISMS IN THE ENHANCER/PROMOTER OF LNCRNAS**

The intronic enhancer of HOTAIR had significantly higher HOTAIR levels in the rs920778 TT genotype than in the CC genotype. By upregulating HOTAIR, the rs920778 TT genotype promotes the development of HBV-related HCC and increases proliferation of HCC cells[97].

LncRNA GAS5 (growth arrest special 5) has been found to be downregulated in HCC patients[98]. A five-base-pair Ins/Del polymorphism (rs145204276) in the promoter region of GAS5 could affect the GAS5 expression. The deletion allele of rs145204276 increases the risk of HBV-related HCC significantly, though the detailed mechanism is unclear[99].

The sequence of RERT-lncRNA overlaps with those of the Ras-related GTP-binding protein 4b and prolyl hydroxylase 1 (EGLN2). An Ins/Del polymorphism (rs10680577) in the distal promoter of RERT-lncRNA may alter the structure of RERT-lncRNA and regulate the expression of RERT-lncRNA and EGLN2. A 4-bp deletion allele of rs10680577 in RERT-lncRNA increases expression of RERT-lncRNA and EGLN2 and promotes the occurrence of HBV-related HCC[100].

**GENETIC POLYMORPHISMS IN THE CODING REGION OF LNCRNAS**

A polymorphism in the coding region of KCNQ1-overlapping transcript 1 (KCNQ1OT1), i.e. rs35622507, may alter the structure of KCNQ1OT1 and modulate the expression of KCNQ1OT1 and cyclin-dependent kinase inhibitor 1C (CDKN1C). The homozygous 10-10 genotype with significantly lower expression of KCNQ1OT1 and higher expression of CDKN1C was shown to increase the risk of HBV-related HCC[101].

LINC01149 variant rs2844512 was identified to facilitate HBV spontaneous recovery but increase the risk of HCC. Further studies indicated this variant created a binding site for miR-128-3p and upregulated MICA expression by serving as a miRNA sponge[102].

**OTHER GENETIC POLYMORPHISMS IN LNCRNAS**

The variant allele of ZNRD1-AS1 (i.e., rs3757328) is reported to associate with HBV clearance[15].

The SNPs in glutamate-ammonia ligase overlapping with LINC00272 were associated with increased risk of HBV-related HCC[103].

Caspase recruitment domain family, member 8 (CARD8) can coordinate innate and adaptive immune responses and may participate in HBV-related HCC. Several SNPs (rs7248320) within a new identified lncRNA AC008392.1, which is located in the upstream region of CARD8 in the long arm of the 9-chromosome, affect the CARD8 expression and may serve as a susceptibility marker for HBV-related HCC[104].

Three regulatory SNPs (rs3757328, rs6940552 and rs9261204) in the ZNRD1-AS1 and the HBV genotype significantly affected HCC susceptibility. The results indicate that ZNRD1-AS1 accompanied by HBV genotypes may influence HCC risk[15].
Tumor necrosis factor receptor superfamily member 10 (TNFRSF10) including TNFRSF10A and TNFRSF10B is a death domain-containing receptor for the apoptotic ligand TNFSF10. In the upstream region of TNFRSF10A and downstream region of TNFRSF10B, IncRNAs RP11-1149O23.3 and RP11-459E5.1 were identified, respectively. The two lncRNAs are possibly involved in the regulation of TNFRSF10A and TNFRSF10B. Several SNPs (i.e., rs79037040-T and rs2058822-A) in RP11-1149O23.3 and RP11-459E5.1 may affect the expression of TNFRSF10A and TNFRSF10B and may be susceptibility markers for HCC and chronic HBV infection.[105]

Paired-box family member PAX8 encodes a transcription factor that may participate in the prognosis of HCC. Several SNPs (rs4848320 and rs1110839) within AC016863.6 lncRNA may affect the PAX8 expression and affect the prognosis of HBV-related HCC.[106]

The association of Inc-RP11-150O12.3 variants (rs2275959, rs1008547, and rs11776545) with HBV-related HCC risk and progression has been reported.[107]

LncRNAs HULC and MALAT1 have been upregulated in HBV-related HCC. Genetic variants of lncRNA HULC (rs7763881) and lncRNA MALAT1 (rs619586) are associated with the decreased susceptibility to HCC.[108]

These studies suggest that genetic polymorphisms in lncRNAs should affect the development and outcome of HBV-related HCC. This may help to identify appropriate targets for prevention and treatment of HCC in the age of personalized medicine.

**REGULATORY MECHANISMS OF LNCRNAS IN HBV REPLICATION AND ONCOGENESIS**

LncRNAs can function as signals, decoys, guides, or scaffolds through interacting with their partner molecules and regulate gene expression at different levels. Up to now, at least seven mechanisms have been found to affect HBV replication and oncogenesis by dysregulated IncRNAs: Epigenetic silencing, transcriptional control, splicing regulation, molecular sponge, production of miRNAs, protein stability modulation, and production of a small polypeptide (Figure 3)[2,109,110].

Epigenetic silencing: Polycomb group (PcG) proteins are epigenetic regulators of transcription. Through multiprotein complexes PRCs, PcGs could modify histones (and other proteins) and silence target genes. LncRNAs may decrease the expression of their target genes through epigenetic silencing either by altering the expression level of PcGs or by interacting with PcGs directly and then silencing their target genes. HOTAIR enhances the degradation of suppressor of Zeste 12 homolog, a key subunit of PRC2, through Ptk1[45]. Several IncRNAs interact with EZH2, a component of PRC2 to modulate (repress in most cases) the expression of their target genes, e.g., HEIH[48], UCA1[53], HOTAIR[47], LINC00152[61], and PVT1[111]. ANRIL can interact with PRC2[112].

Transcriptional control: LncRNAs can activate the transcription of their target genes in cis or in trans. HOTITIP could promote the expression of its neighboring homeobox A genes (HOAX genes) in HCC [57]. LINC00152 binds to the promoters of epithelial cell adhesion molecule and IL-23 to activate their transcription in HCC patients[113]. MALAT1 could up-regulate the expression of LTBP3[63].

Splicing regulation: LncRNAs could affect the expression of their target genes through alternative splicing regulation. MALAT1, a nuclear lncRNA, could interact with the SR proteins (serine/arginine-rich family of nuclear phosphoproteins) and change the cellular levels of the phosphorylated forms of SR proteins to modulate alternative splicing in HCC[62].

Molecular sponge: LncRNAs could exert their effects by acting as molecular sponges for miRNAs, i.e., competitive endogenous RNA (ceRNA)[114]. Through molecular sponges, IncRNAs sequester miRNAs and then de-repress the expression of the miRNA target genes. Several IncRNAs, such as Unigene56159 [69], HULC[115], HBx-LINE1[16], UCA1[55], ANRIL[60], LINC0149 variant[102], LINC01352[93], F11-AS1[94], LINC01352[70], n335586[73], XIST[74], SNHG5[75], SSTR5-AS1[116], and TRERNA1[79] are involved in the development of HBV-related HCC by sequestering miRNAs.

Production of miRNAs: LncRNAs could produce miRNAs to regulate their target genes by serving as precursors of miRNAs. The Ftx transcript encodes two clusters of miRNAs (i.e., miR-374a and miR-545) in its introns in HBV-related HCC[117].

Protein stability modulation: LncRNAs could stabilize their protein targets by direct interactions. LncRNA-Dreh could bind vimentin, a type III intermediate filament, and stabilize its filament structure [84]. LncRNAs could also stabilize their protein targets by reduced degradation of these proteins indirectly. By enhancing ubiquitin-specific peptidase 22, HULC suppresses ubiquitin-mediated degradation of cyclooxygenase-2 and silent information regulator 1 in HCC[118].

Production of a small polypeptide: A putative lncRNA HBVPTPAP could encode a small polypeptide to induce the apoptosis of HCC cells[110].

Through these different mechanisms, IncRNAs can regulate gene expression. As more IncRNAs are identified, more novel mechanisms will be revealed.
Figure 3 Regulatory mechanisms of various long noncoding RNAs in hepatitis B virus replication and oncogenesis[2]. A: HOX transcript antisense RNA (HOTAIR), high expression in hepatocellular carcinoma, urothelial carcinoma associated 1 (UCA1), HOTAIR, LINCO0152, PVT1, and antisense noncoding RNA in the INK4 locus (ANRIL) could regulate gene expression through epigenetic silencing; B: HOXA transcript at the distal tip, LINCO0152, and metastasis associated in lung adenocarcinoma transcript 1 (MALAT1) could increase the expression of their target genes through transcriptional control; C: MALAT1 could modulate alternative splicing; D: Unigene56159, highly upregulated in liver cancer (HULC), hepatitis B virus (HBV) X protein-long interspersed nuclear elements 1, UCA1, ANRIL, LINCO11149 variant, LINCO1352, F11-AS1, LINCO1232, n335568, XIST, SNHG5, SSTR5-AS1, and TRERNA1 regulate the gene expression through molecular sponging to sequester miRNAs; E: Long noncoding RNAs (lncRNAs) Ftx could produce miRNAs to regulate their target genes; F: LncRNA-Dreh and HULC could modulate protein stability; G: LncRNA HBVPTPAP could encode a small polypeptide to exert its function.

LncRNAs as Potential Biomarkers for Diagnosis and Therapy of HBV-Related HCC

It is suggested that HOTAIR may potentially be a novel HBV diagnostic biomarker based on its ability to facilitate HBV transcription and replication. This may not be practical because the commercially available diagnostic kits for HBV infection already have high specificities and sensitivities. On the other hand, the specificity and sensitivity of currently available tumor markers for HBV-related HCC (e.g., α-fetoprotein) are not sufficient. This results in the poor prognosis of HBV-related HCC. This has encouraged researchers to search for novel potential biomarkers of HCC. Various miRNAs have been accepted to be biomarkers for diagnosis and therapy for HCC[119]. As an increasing number of lncRNAs, as well as the genetic polymorphisms in lncRNAs, have been found to contribute in the development of HBV-related HCC, researchers have tried to study whether these lncRNAs could be used as novel biomarkers for HBV-related HCC[120]. To be tumor markers, lncRNAs have the advantage over proteins because they can be amplified easily, e.g., by RT-PCR. A number of lncRNAs dysregulated in HBV-related HCC have been suggested to be potential markers for HCCs. If these lncRNAs can be secreted to biological fluids, e.g., blood, they can be easily detected. Therefore, those secreted lncRNAs are suggested to be potential markers for HBV-related HCC, such as HULC[121], IGF2AS[122], Linc00152[121], IncRNA-uc003wbd[123], IncRNA-AF085935[123], uc001ncr[124], AX800134[124], and UCA1[53-55]. However, most of these circulating lncRNAs aberrantly expressed in HBV-related HCC are also dysregulated in other tumors. It is better to identify a circulating lncRNA specific for HBV-related HCC diagnosis[125]. Alternatively, detection of several lncRNAs together could be an option[126-130].
Gene therapies such as RNA interference may become a common treatment for HCC in the future. In this way, IncRNAs can be the new therapeutic targets for HBV-related HCC. It is reported that metformin can suppress the HULC expression and block the progression of HBV-related HCC[131]. Thus, HULC could be a potential therapeutic target for RNA interference in HBV-related HCC treatment. Other IncRNAs upregulated in HBV-related HCC are also reported to be potential therapeutic targets[8], such as MVIH[68] and HBx-LINE1[16]. On the other hand, an effective way to deliver IncRNA MEG3 RNA using MS2 virus-like-particles to inhibit HCC cells has been developed [132]. Other IncRNAs downregulated in HBV-related HCC could use a similar approach to treat HBV-related HCC, such as DREH[84] and LET[85]. Other advances in gene and epigenetic editing will enable correcting the aberrations caused by the dysregulated IncRNAs in HBV-related HCC in the future.

CONCLUSION

The important roles of IncRNAs in HBV replication and oncogenesis have started to emerge in recent years. Growing evidence indicates that some IncRNAs are dysregulated in HBV-infected cells and/or HBV-related HCC. Functional characterization of these IncRNAs has led to a more comprehensive understanding of HBV replication and oncogenesis. These IncRNAs have diverse functions, which are now beginning to be revealed. Although the progress regarding the role of IncRNAs in HBV-related HCC has been impressive, their roles in HBV replication, host immune responses, and HBV-related chronic diseases need further characterization. Even in HBV-related HCC, only a small part of IncRNAs has been well characterized, and a large portion of IncRNAs remains to be further explored. Thus, more efforts are required to understand the detailed mechanisms of these IncRNAs in the progression of HCC. The growing studies on the roles of IncRNAs in hepatocarcinogenesis could result in designing LncRNAs as potential biomarkers for diagnosis and therapy of HBV-related HCC.

Several technologies such as chromatin immunoprecipitation (ChIP), RNA sequencing, ChIP sequencing, tiled RNA expression arrays, cap analysis of gene expression, and serial analysis of gene expression have been used to detect IncRNAs. Only recently, different types of post-transcriptional chemical modifications of RNAs have been detected and characterized through sequencing-based, transcriptome-wide studies, e.g., pseudouridine (Ψ), N6-methyladenosine and 5-methylcytosine. These modifications have been shown to affect the fate of RNA, including IncRNAs[133]. Further details about the roles of these chemical modifications of IncRNAs in HBV replication and oncogenesis are expected in the near future.

FOOTNOTES

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